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Query Match	35.54	Score 723.5	DB 3	Length 359
Best Local Similarity	39.08	Pred. No. 1.2e+5		
Matches 142	Conservative 65	Mismatches 127	Indels 35	Gaps 7

[illegible]

RESULT: 1  
 Status: 5 Application in progress  
 3-14-68 No. 610,500  
 GENERAL COMMENTS: MICHAEL  
 APPLICANT TESTED, TRAINED  
 APPLICANT MICHAEL HALL  
 NUMBER OF SIGHTINGS: 5  
 ADDRESS: 5140000  
 STREET: P.O. BOX 480  
 CITY: VALLEY FORD  
 COUNTY: INDIANA  
 ZIP: 44424  
 COMMENTS: RELIABLE SOURCE  
 COMMENTS: FBI Acceptable

[illegible]

FILE# 44169  
INFORMATION FIP SEQ ID NO 6  
SEQUENCE CHARACTERISTICS

1. LINDH, J. B. *Medicinal plants of the*  
 2. *Sierr Leone*.  
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1. NAME : JOHN J. WATSON  
 2. DATE OF BIRTH : 12/15/1942  
 3. SEX : M  
 4. EDUCATION : HS  
 5. RELIGION : PROTESTANT  
 6. ETHNICITY : WHITE  
 7. HEIGHT : 5'10"  
 8. WEIGHT : 175  
 9. HAIR : BROWN  
 10. EYES : BROWN  
 11. SCARS : NO  
 12. TOOTH : NO  
 13. MARKS : NO  
 14. GLASSES : NO  
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 16. HAIR STYLE : SHORT  
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Wed Apr 23 07:41:00 2003

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Page 9

Search completed: April 22, 2003, 16:42:57  
Data time: 37 secs



1 PRIOR FILING DATE 1997-11-03  
 2 PRIOR APPLICATION NUMBER 65/755311  
 3 PRIOR FILING DATE 1997-11-13  
 4 PRIOR APPLICATION NUMBER 65/755364  
 5 PRIOR FILING DATE 1997-11-21  
 6 PRIOR APPLICATION NUMBER 65/774520  
 7 PRIOR FILING DATE 1998-03-11  
 8 PRIOR APPLICATION NUMBER 65/773641  
 9 PRIOR FILING DATE 1998-03-11  
 10 PRIOR APPLICATION NUMBER 65/776639  
 11 PRIOR FILING DATE 1998-03-12  
 12 PRIOR APPLICATION NUMBER 65/778866  
 13 PRIOR FILING DATE 1998-03-20  
 14 PRIOR APPLICATION NUMBER 65/778936  
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 16 PRIOR APPLICATION NUMBER 65/778910  
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 19 PRIOR FILING DATE 1998-03-26  
 20 PRIOR APPLICATION NUMBER 65/779664  
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 28 PRIOR APPLICATION NUMBER 65/782500  
 29 PRIOR FILING DATE 1998-03-30  
 30 PRIOR APPLICATION NUMBER 65/782505  
 31 PRIOR FILING DATE 1998-03-31  
 32 PRIOR APPLICATION NUMBER 65/786165  
 33 PRIOR FILING DATE 1998-03-31  
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1 APPLICANT: Gaddard, Audrey  
 2 APPLICANT: Gaddard, Audrey  
 3 APPLICANT: Gammill, Christopher  
 4 APPLICANT: Gurney, Austin L.  
 5 APPLICANT: Hahn, Kenneth J.  
 6 APPLICANT: Hahn, Kenneth J.  
 7 APPLICANT: Koo, Sophia S.  
 8 APPLICANT: Miller, Mary A.  
 9 APPLICANT: Miller, Mary A.  
 10 APPLICANT: Pimentel, Nicholas P.  
 11 APPLICANT: Pimentel, Nicholas P.  
 12 APPLICANT: Street, Timothy A.  
 13 APPLICANT: Street, Timothy A.  
 14 APPLICANT: Thomas, Daniel  
 15 APPLICANT: Williams, Mickey  
 16 APPLICANT: Williams, Mickey  
 17 TITLE OF INVENTION: Amino Acid Encoded Lip Name  
 18 CURRENT FILING DATE: 2001-10-19  
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OM protein - protein search, using sw model:

Run on: April 22, 2003, 16:28:42 ; Search time 25 Seconds

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Scoring table: BLASTSUM62  
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Searched: 112892 seqs, 41476328 residues

	Total number of fits satisfying chosen parameters
(a)	112692

Minimum DB seq length: 7

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Maximum Match 100%

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ried: no. is the number of  
score greater than or equal

ped No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Serial No.	Score	Count	Match	Length	DB	ID	Description
1	2035	106,0	470	1	NH1	MOJAN	P04728 from seq1
2	2021	99,1	370	1	NH1	MOJSE	P04728 from seq1
3	2021	99,1	370	1	NH1	MOJSE	P04728 from seq1
4	1555	78,1	370	1	NH1	MOJSE	P04728 from seq1
5	1469	71,5	371	1	NH1	MOJSE	P21016 from seq1
6	1092,5	57,2	466	1	NH1	MOJSE	P22676 from seq1
7	1092,5	57,2	466	1	NH1	MOJSE	P22676 from seq1
8	443,5	41,4	352	1	NH1	MOJSE	P22676 from seq1
9	443,5	41,4	352	1	NH1	MOJSE	P22676 from seq1
10	443,5	41,4	352	1	NH1	MOJSE	P22676 from seq1
11	443,5	41,4	352	1	NH1	MOJSE	P22676 from seq1
12	443,5	41,4	352	1	NH1	MOJSE	P22676 from seq1
13	443,5	41,4	352	1	NH1	MOJSE	P22676 from seq1
14	443,5	41,4	352	1	NH1	MOJSE	P22676 from seq1
15	443,5	41,4	352	1	NH1	MOJSE	P22676 from seq1
16	443,5	41,4	352	1	NH1	MOJSE	P22676 from seq1
17	443,5	41,4	352	1	NH1	MOJSE	P22676 from seq1
18	443,5	41,4	352	1	NH1	MOJSE	P22676 from seq1
19	443,5	41,4	352	1	NH1	MOJSE	P22676 from seq1
20	443,5	41,4	352	1	NH1	MOJSE	P22676 from seq1
21	443,5	41,4	352	1	NH1	MOJSE	P22676 from seq1
22	443,5	41,4	352	1	NH1	MOJSE	P22676 from seq1
23	443,5	41,4	352	1	NH1	MOJSE	P22676 from seq1
24	443,5	41,4	352	1	NH1	MOJSE	P22676 from seq1
25	443,5	41,4	352	1	NH1	MOJSE	P22676 from seq1
26	443,5	41,4	352	1	NH1	MOJSE	P22676 from seq1
27	443,5	41,4	352	1	NH1	MOJSE	P22676 from seq1
28	443,5	41,4	352	1	NH1	MOJSE	P22676 from seq1
29	443,5	41,4	352	1	NH1	MOJSE	P22676 from seq1
30	443,5	41,4	352	1	NH1	MOJSE	P22676 from seq1
31	754,5	37,2	350	1	NH1A	MOJAN	P31160 xenopus laevis

## ALIGNMENTS

[illegible]

Matches 370: Conservative 0: Mismatches 0: Indels 0: Gap 0:  
 0Y 1 MGLPILPAPVATLALAAAPALAAASPPKALVAVASNTLITGSLQVLES 40  
 1 MGLPILPAPVATLALAAAPALAAASPPKALVAVASNTLITGSLQVLES 40  
 0Y 1 MGLPILPAPVATLALAAAPALAAASPPKALVAVASNTLITGSLQVLES 40  
 61 LGLLSMVELLPHQWVLIHSVSGVAVKWCWQWQWQWQWQWQWQWQWQ 120  
 61 LGLLSMVELLPHQWVLIHSVSGVAVKWCWQWQWQWQWQWQWQWQWQ 120  
 0Y 121 CREATIVIAADAVIVAVKSCSISCTCQVPPVPIHVMQWQWQWQWQ 180  
 121 CREATIVIAADAVIVAVKSCSISCTCQVPPVPIHVMQWQWQWQWQ 180  
 0Y 181 GREVVSCHQKULATLHMKADATVWQDQVCHQVNSCTYPTQWQWQ 240  
 181 GREVVSCHQKULATLHMKADATVWQDQVCHQVNSCTYPTQWQWQ 240  
 0Y 241 ACDVQVPPQVQVAVYVPSVAVASVLIPLKLPVAVPSPVQVQVQV 300  
 241 ACDVQVPPQVAVYVPSVAVASVLIPLKLPVAVPSPVQVQVQV 300  
 0Y 301 YQGLAQVLAQVAVASVAVVQVNSVAVASVLIPLKLPVAVPSPVQV 360  
 301 YQGLAQVLAQVAVASVAVVQVNSVAVASVLIPLKLPVAVPSPVQV 360  
 0Y 361 THTVAVQV 370  
 361 THTVAVQV 370  
 0Y 370 THTVAVQV 370  
 370 THTVAVQV 370

RESULT 2  
 WNT1-MOUSE  
 ID WNT1-MOUSE STANDARD PRT. 370 AA  
 DT 13-AUG-1987 (rel. 05, Cleaved)  
 DT 13-AUG-1987 (rel. 05, last sequence update)  
 DE WNT1 protein sequence from mouse embryo  
 GN WNT1 (WNT1) (1-370)  
 OS Mus musculus (mouse)  
 OC Eukaryota; Chordata; Eumetazoa; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Soricomorpha; Muridae; Murinae; Mus  
 NC NC01\_263010 (070)  
 RX NC01\_263010 (070)  
 RP SEQUENCE FROM N A  
 RC STRAIN:CH1  
 RA Cooper N.V. Nuss R.  
 RT Structure and nucleotide sequence of the putative tumorigenic  
 infect. proviral insertions have the protein-encoding domain  
 Cell 39:233-241 (1984).

WNT1-MOUSE  
 ID WNT1-MOUSE STANDARD PRT. 370 AA  
 DT 13-AUG-1987 (rel. 05, Cleaved)  
 DT 13-AUG-1987 (rel. 05, last sequence update)  
 DE WNT1 protein sequence from mouse embryo  
 GN WNT1 (WNT1) (1-370)  
 OS Mus musculus (mouse)  
 OC Eukaryota; Chordata; Eumetazoa; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Soricomorpha; Muridae; Murinae; Mus  
 NC NC01\_263010 (070)  
 RX NC01\_263010 (070)  
 RP SEQUENCE FROM N A  
 RC STRAIN:CH1  
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 RT Structure and nucleotide sequence of the putative tumorigenic  
 infect. proviral insertions have the protein-encoding domain  
 Cell 39:233-241 (1984).

severe abnormalities in midline and cerebellar development.  
 NC01\_263010 (070)  
 DE WNT1 protein sequence from mouse embryo  
 GN WNT1 (WNT1) (1-370)  
 OS Mus musculus (mouse)  
 OC Eukaryota; Chordata; Eumetazoa; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Soricomorpha; Muridae; Murinae; Mus  
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 Cell 39:233-241 (1984).

WNT1-MOUSE  
 ID WNT1-MOUSE STANDARD PRT. 370 AA  
 DT 13-AUG-1987 (rel. 05, Cleaved)  
 DT 13-AUG-1987 (rel. 05, last sequence update)  
 DE WNT1 protein sequence from mouse embryo  
 GN WNT1 (WNT1) (1-370)  
 OS Mus musculus (mouse)  
 OC Eukaryota; Chordata; Eumetazoa; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Soricomorpha; Muridae; Murinae; Mus  
 NC NC01\_263010 (070)  
 RX NC01\_263010 (070)  
 RP SEQUENCE FROM N A  
 RC STRAIN:CH1  
 RA Cooper N.V. Nuss R.  
 RT Structure and nucleotide sequence of the putative tumorigenic  
 infect. proviral insertions have the protein-encoding domain  
 Cell 39:233-241 (1984).

WNT1-MOUSE  
 ID WNT1-MOUSE STANDARD PRT. 370 AA  
 DT 13-AUG-1987 (rel. 05, Cleaved)  
 DT 13-AUG-1987 (rel. 05, last sequence update)  
 DE WNT1 protein sequence from mouse embryo  
 GN WNT1 (WNT1) (1-370)  
 OS Mus musculus (mouse)  
 OC Eukaryota; Chordata; Eumetazoa; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Soricomorpha; Muridae; Murinae; Mus  
 NC NC01\_263010 (070)  
 RX NC01\_263010 (070)  
 RP SEQUENCE FROM N A  
 RC STRAIN:CH1  
 RA Cooper N.V. Nuss R.  
 RT Structure and nucleotide sequence of the putative tumorigenic  
 infect. proviral insertions have the protein-encoding domain  
 Cell 39:233-241 (1984).





















```
Db 231 VAKKTCNTVRSKSTKV-----LPPKSSPHATCEVTLSSPFL 346
Oy 305 LQPMZAGANSSSALDZELZCRHPTPOVTLN-TPMKCWSHNP 311 344
Db 286 NQVTSRQNTSALOG-ELMCCGRHTRVAVKSSPHMCCSWCKE 343 345
Oy 355 VLEDC 343
Db 346 ETHPC 350

Search completed: April 23, 2003 10:39:47
Job time : 26 secs
```

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Genbank version: 5.1.4.05.1578  
Copyright (c) 1991 - 2001 Compendex Ltd.

OM protein - Protein search, using SW model:

Run on: April 23, 2003, 16:36:48 : Search time: 37 seconds

US-09-674-292-1

Target protein score: 2295

Sequence: 1 NQALMLCHMSWTLMLALA... WYNSWYTRFWLML 370

Scoring table: Gap: 10.0 : Expect: 0.5

Search: 67150 seqs, 2604215 residues

Total number of hits satisfying chosen parameters: 67146

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum match: 100

Listing first 45 similarities

Databases:

SPRINT-21:  
1. sp.archaea  
2. sp.bacteria  
3. sp.fungi  
4. sp.human  
5. sp.invertebrate  
6. sp.mammalia  
7. sp.plant  
8. sp.primates  
9. sp.reptiles  
10. sp.insecta  
11. sp.rodent  
12. sp.rodent  
13. sp.rodent  
14. sp.rodent  
15. sp.rodent  
16. sp.rodent  
17. sp.rodent

Prod No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SIMILARITIES

Result No.	Score	Accession	DB ID	Description
1	2295	U00001	1	Escherichia coli
2	1131.5	U00001	2	Escherichia coli
3	1131.5	U00001	3	Escherichia coli
4	1131.5	U00001	4	Escherichia coli
5	1131.5	U00001	5	Escherichia coli
6	1131.5	U00001	6	Escherichia coli
7	1131.5	U00001	7	Escherichia coli
8	1131.5	U00001	8	Escherichia coli
9	1131.5	U00001	9	Escherichia coli
10	1131.5	U00001	10	Escherichia coli
11	1131.5	U00001	11	Escherichia coli
12	1131.5	U00001	12	Escherichia coli
13	1131.5	U00001	13	Escherichia coli
14	1131.5	U00001	14	Escherichia coli
15	1131.5	U00001	15	Escherichia coli

12	109.5	U00001	12	Escherichia coli
13	109.5	U00001	13	Escherichia coli
14	109.5	U00001	14	Escherichia coli
15	109.5	U00001	15	Escherichia coli
16	109.5	U00001	16	Escherichia coli
17	109.5	U00001	17	Escherichia coli
18	109.5	U00001	18	Escherichia coli
19	109.5	U00001	19	Escherichia coli
20	109.5	U00001	20	Escherichia coli
21	109.5	U00001	21	Escherichia coli
22	109.5	U00001	22	Escherichia coli
23	109.5	U00001	23	Escherichia coli
24	109.5	U00001	24	Escherichia coli
25	109.5	U00001	25	Escherichia coli
26	109.5	U00001	26	Escherichia coli
27	109.5	U00001	27	Escherichia coli
28	109.5	U00001	28	Escherichia coli
29	109.5	U00001	29	Escherichia coli
30	109.5	U00001	30	Escherichia coli
31	109.5	U00001	31	Escherichia coli
32	109.5	U00001	32	Escherichia coli
33	109.5	U00001	33	Escherichia coli
34	109.5	U00001	34	Escherichia coli
35	109.5	U00001	35	Escherichia coli
36	109.5	U00001	36	Escherichia coli
37	109.5	U00001	37	Escherichia coli
38	109.5	U00001	38	Escherichia coli
39	109.5	U00001	39	Escherichia coli
40	109.5	U00001	40	Escherichia coli
41	109.5	U00001	41	Escherichia coli
42	109.5	U00001	42	Escherichia coli
43	109.5	U00001	43	Escherichia coli
44	109.5	U00001	44	Escherichia coli
45	109.5	U00001	45	Escherichia coli

ALIGNMENTS

1	U00001	1	Escherichia coli
2	U00001	2	Escherichia coli
3	U00001	3	Escherichia coli
4	U00001	4	Escherichia coli
5	U00001	5	Escherichia coli
6	U00001	6	Escherichia coli
7	U00001	7	Escherichia coli
8	U00001	8	Escherichia coli
9	U00001	9	Escherichia coli
10	U00001	10	Escherichia coli
11	U00001	11	Escherichia coli
12	U00001	12	Escherichia coli
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15	U00001	15	Escherichia coli
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36	U00001	36	Escherichia coli
37	U00001	37	Escherichia coli
38	U00001	38	Escherichia coli
39	U00001	39	Escherichia coli
40	U00001	40	Escherichia coli
41	U00001	41	Escherichia coli
42	U00001	42	Escherichia coli
43	U00001	43	Escherichia coli
44	U00001	44	Escherichia coli
45	U00001	45	Escherichia coli



DB 370. |||||||.....|||

394

# RESULT 4

ID Q01356 PELICINARITY PRG 374 AA

AC Q01356 PELICINARITY 21 (GenBank)

CT 01-JUN-2002 (JEMBLER) 21 (Last sequence update)

DT 01-JUN-2002 (JEMBLER) 21 (Last modification date)

## Matches

08 Caprenitum aalei (Manduca spidei)

09 Eukalypta, Melazon Atropocia, Melicocera, Acanthula, Alucace

0X NCBI:taxid=9528

0X MEDLINE:141363 PubMed:1487439

0X MEDLINE:141363 PubMed:1487439

0X MEDLINE:141363 PubMed:1487439

0X MEDLINE:141363 PubMed:1487439

0X MEDLINE:141363 PubMed:1487439

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